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<110> Johansen, Teit E.  
Wen-Yee Saw, Dinah

<110> Novel Neurotrophic Factors

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<140> U.S.S.N 09/804,615

<141> 2001-03-12

<150> DANISH 1998 00904

<151> 1998-07-06

<150> USSN 60/092,229

<151> 1998-07-09

<150> DANISH 1998 01048

<151> 1998-08-19

<150> USSN 60/097,774

<151> 1998-08-25

<150> USSN 60/103,908

<151> 1998-10-13

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<151> 1998-10-06

<150> U.S.S.N 09/347,613

<151> 1999-07-02

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<170> PatentIn Ver. 2.1

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<223> CARBOHYD: Glycosylated Asparagine at Asn87

<220>

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<220> (426)..(623)

<223> DISULFID - Cys3-Cys73 disulfide bridge

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<220> (507)..(707)

<223> DISULFID: Cys35-Cys101 disulfide bridge

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<223> DISULFID: Cys39-Cys103 disulfide bridge

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<223> DISULFID: Cys72-Cys72 interchain disulfide bridge

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tcccgaagcc caccctgggtg cccctctttct ccccgaggct ccacttggtc tctccgcgc 119

atg cct gcc ctg tgg ccc acc ctg gcc gct ctg gct ctg ctg agc agc 167

Met Pro Ala Leu Trp Pro Thr Leu Ala Ala Leu Ala Leu Leu Ser Ser

-75

-90

-85

-80

gtc gca gag gcc tcc ctg ggc tcc gag ccc ccg agc cct gcc ccc ccg	215
Val Ala Glu Ala Ser Leu Gly Ser Ala Pro Arg Ser Pro Ala Pro Arg	
-75 -70 -65	
gaa ggc ccc ccg cct gtc ctg gag tcc ccc gcc ggc ccc ctg ccg ggg	263
Glu Gly Pro Pro Pro Val Leu Ala Ser Pro Ala Gly His Leu Pro Gly	
-60 -55 -50	
gga ccg acc gcc ccg tgg tgc agt gga aga gcc ccg ccg ccg ccg ccg	311
Gly Arg Thr Ala Arg Trp Cys Ser Gly Arg Ala Arg Arg Pro Arg Arg	
-45 -40 -35	
aga ccc ttc tcg gcc ccg gcc ccc gcc gcc tgc acc ccc atc tgc tct	359
Arg His Phe Ser Ala Arg Ala Pro Ala Ala Cys Thr Pro Ile Cys Ser	
-30 -25 -20	
tcc ccg ccg gtc ccg gag gag ccg ctg ggg gcc ccg gca gag ccg tcg	407
Ser Pro Arg Val Arg Ala Ala Arg Leu Gly Gly Arg Ala Ala Arg Ser	
-15 -10 -5 -1 1	
ggc agc ggg gcc gag ggg tgc ccg ctg ccg tcg ccg ctg gtc ccg gtc	455
Gly Ser Gly Gly Ala Gly Cys Arg Leu Arg Ser Gln Leu Val Pro Val	
5 10 15	
ccg gag ctc gcc ctg gcc ccc ccg tcc gac gag ctg gtc cgt ttc ccg	503
Arg Ala Leu Gly Leu Gly His Arg Ser Asp Glu Leu Val Arg Phe Arg	
20 25 30	
ttc tgc acc gcc tcc tgc ccg ccg gag ccg tct cca ccc gac ctc agc	551
Phe Cys Thr Gly Ser Cys Pro Arg Ala Arg Ser Pro His Asp Leu Ser	
35 40 45	
ctg gcc agc cta ctg gcc gcc ggg gcc ctg cga ccg ccc ccg gcc tcc	599
Leu Ala Ser Leu Leu Gly Ala Gly Ala Leu Arg Pro Pro Pro Gly Ser	
50 55 60 65	
ccg ccc gtc agc ccg ccc tgc tgc cga ccc acc ccg ccg tac gaa gag gtc	647
Arg Pro Val Ser Gln Pro Cys Cys Arg Pro Thr Arg Tyr Glu Ala Val	
70 75 80	
tcc ttc atg gac gtc aac agc acc tgg aga acc gtc gac ccg ctc tcc	695
Ser Phe Met Asp Val Asn Ser Thr Trp Arg Thr Val Asp Arg Leu Ser	
85 90 95	
gcc acc gcc tgc gcc tgc ctg gcc tgaggggctcg ctccagggtt ttgcagactg	749
Ala Thr Ala Cys Gly Cys Leu Gly	
100 105	

gaccattacc ggtggctctt cctgctggg accctccgc agagtccac tagccaggg 809  
 cctcagccag ggaaggaagg ctcaaagctg agaggccct gccggtgggt gatgga 865

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Val Ala Glu Ala Ser Leu Gly Ser Ala Pro Arg Ser Pro Ala Pro Arg  
 -75 -70 -65

Glu Gly Pro Pro Pro Val Leu Ala Ser Pro Ala Gly His Leu Pro Gly  
 -60 -55 -50

Gly Arg Thr Ala Arg Trp Cys Ser Gly Arg Ala Arg Arg Pro Arg Arg  
 -45 -40 -35

Arg His Phe Ser Ala Arg Ala Pro Ala Ala Cys Thr Pro Ile Cys Ser  
 -30 -25 -20

Ser Pro Arg Val Arg Ala Ala Arg Leu Gly Gly Arg Ala Ala Arg Ser  
 -15 -10 -5 -1 1

Gly Ser Gly Gly Ala Gly Cys Arg Leu Arg Ser Gln Leu Val Pro Val  
 5 10 15

Arg Ala Leu Gly Leu Gly His Arg Ser Asp Glu Leu Val Arg Phe Arg  
 20 25 30

Phe Cys Thr Gly Ser Cys Pro Arg Ala Arg Ser Pro His Asp Leu Ser  
 35 40 45

Leu Ala Ser Leu Leu Gly Ala Gly Ala Leu Arg Pro Pro Pro Gly Ser  
 50 55 60 65

Arg Pro Val Ser Gln Pro Cys Cys Arg Pro Thr Arg Tyr Glu Ala Val  
 70 75 80

Ser Phe Met Asp Val Asn Ser Thr Trp Arg Thr Val Asp Arg Leu Ser  
 85 90 95

Ala Thr Ala Cys Gly Cys Leu Gly

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 <223> DISULFID: Cys43-Cys108 disulfide bridge

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 <222> (505)..(705)  
 <223> DISULFID: Cys70-Cys136 disulfide bridge

<220>  
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 <222> (517)..(711)  
 <223> DISULFID: Cys74-Cys138 disulfide bridge

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 <223> DISULFID: Cys107-Cys107 interchain disulfide  
 bridge

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 Met Pro Gly Leu Ile Ser Ala Arg Gly Gln Pro Leu Leu Glu  
 -95 -90 -85

gtc ctt cct ccc caa gcc cac ctg ggt gcc ctg ttt ctg cct gag gct 96  
 Val Leu Pro Pro Gln Ala His Leu Gly Ala Leu Phe Leu Pro Glu Ala  
 -30 -75 -70

cca ctt ggt ctg tcc ggc cag cct gcc ctg tgg ccc acc ctg gcc gct 144  
 Pro Leu Gly Leu Ser Ala Gln Pro Ala Leu Trp Pro Thr Leu Ala Ala  
 -65 -60 -55

ctg gct ctg ctg agc agc gtc gca gag gcc tcc ctg ggc tcc ggc ccc 192  
 Leu Ala Leu Leu Ser Ser Val Ala Glu Ala Ser Leu Gly Ser Ala Pro  
 -50 -45 -40

ggc agc cct gcc ccc cgc gaa ggc ccc cgc cct gtc ctg ggc tcc ccc 240  
 Arg Ser Pro Ala Pro Arg Glu Gly Pro Pro Pro Val Leu Ala Ser Pro  
 -35 -30 -25 -20

gcc ggc cac ctg cgc ggc gga cgc acg gcc cgc tgg tgc agt gga aga 288  
 Ala Gly His Leu Pro Gly Gly Arg Thr Ala Arg Trp Cys Ser Gly Arg  
 -15 -10 -5

gcc cgc cgc cgc cgc cgc cag cct tct cgc ccc ggc ccc cgc cgc cct 336  
 Ala Arg Arg Pro Pro Pro Gln Pro Ser Arg Pro Ala Pro Pro Pro Pro  
 -1 1 5 10

gca ccc cca tct gct ctt ccc cgc ggc ggc cgc ggc ggc cgc gct ggc 384  
 Ala Pro Pro Ser Ala Leu Pro Arg Gly Gly Arg Ala Ala Arg Ala Gly  
 15 20 25

ggc ccg ggc aac cgc gct cgg qca ggc ggg ggc cgg ggc tgc cgc ctg 432  
 Gly Pro Gly Asn Arg Ala Arg Ala Ala Gly Ala Arg Gly Cys Arg Leu  
 30 35 40 45

cgc tgc cag ctg gtg ccg gtg cgc ggc ctg ggc cgc cgc cgc tgc 480  
 Arg Ser Gln Leu Val Pro Val Arg Ala Leu Gly Leu Gly His Arg Ser  
 50 55 60

gac gag ctg gtg cgt ttc cgc ttc tgc agc ggc tgc tgc cgc cgc ggc 528  
 Asp Glu Leu Val Arg Phe Arg Phe Cys Ser Gly Ser Cys Arg Arg Ala  
 65 70 75

cgc tct cca cac gac ctg agc ctg gcc agc cta ctg ggc gcc ggc gcc 576  
 Arg Ser Pro His Asp Leu Ser Leu Ala Ser Leu Leu Gly Ala Gly Ala  
 80 85 90

ctg cga ccg ccg ccg ggc tgc ccg ccg gtc agc cag ccg tgc tgc cga 624  
 Leu Arg Pro Pro Pro Gly Ser Arg Pro Val Ser Gln Pro Cys Cys Arg  
 95 100 105

ccc acc cgc tac gaa ggc gtc tgc ttc atg gac gtc aac agc acc tgg 672  
 Pro Thr Arg Tyr Glu Ala Val Ser Phe Met Asp Val Asn Ser Thr Trp  
 110 115 120 125

aga acc gtg gac cgc ctg tgc gcc aac ccg tgc ggc tgc ctg ggc 717  
 Arg Thr Val Asp Arg Leu Ser Ala Asn Pro Cys Gly Cys Leu Gly  
 130 135 140

tgagggtctg ctccagggt ttgcagaatg gacccattacc ggtggctctt cctgcctggg 777

accctccgc agagtccac tagccaggg cctcagccag ggacgaagga ctcaaagctg 837

agaggccct gccgggtgggt gatg 861

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<211> 237

<212> PRT

<213> Homo sapiens

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 -80 -75 -70

Gly Leu Ser Ala Gln Pro Ala Leu Trp Pro Thr Leu Ala Ala Leu Ala

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Leu Leu Ser Ser Val Ala Glu Ala Ser Leu Gly Ser Ala Pro Arg Ser						
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Pro Ala Pro Arg Glu Gly Pro Pro Pro Val Leu Ala Ser Pro Ala Gly						
	-30		-25		-20	
His Leu Pro Gly Gly Arg Thr Ala Arg Trp Cys Ser Gly Arg Ala Arg						
	-15		-10		-5	
Arg Pro Pro Pro Gln Pro Ser Arg Pro Ala Pro Pro Pro Pro Ala Pro						
-1 1 5 10 15						
Pro Ser Ala Leu Pro Arg Gly Gly Arg Ala Ala Arg Ala Gly Gly Pro						
	20		25		30	
Gly Asn Arg Ala Arg Ala Ala Gly Ala Arg Gly Cys Arg Leu Arg Ser						
	35		40		45	
Gln Leu Val Pro Val Arg Ala Leu Gly Leu Gly His Arg Ser Asp Glu						
	50		55		60	
Leu Val Arg Phe Arg Phe Cys Ser Gly Ser Cys Arg Arg Ala Arg Ser						
	65		70		75	
Pro His Asp Leu Ser Leu Ala Ser Leu Leu Gly Ala Gly Ala Leu Arg						
	80		85		90	95
Pro Pro Pro Gly Ser Arg Pro Val Ser Gln Pro Cys Cys Arg Pro Thr						
	100		105		110	
Arg Tyr Glu Ala Val Ser Phe Met Asp Val Asn Ser Thr Trp Arg Thr						
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Val Asp Arg Leu Ser Ala Asn Pro Cys Gly Cys Leu Gly						
	130		135		140	

<210> 5

<211> 140

<212> PRT

<213> Homo sapiens

<220>

<223> Wherein Xaa at position 134 designates Asn or Thr,  
and Xaa at position 135 designates Ala or Pro



<400> 5

Pro Pro Pro Gln Pro Ser Arg Pro Ala Pro Pro Pro Pro Ala Pro Pro  
1 5 10 15

Ser Ala Leu Pro Arg Gly Gly Arg Ala Ala Arg Ala Gly Gly Pro Gly  
20 25 30

Asn Arg Ala Arg Ala Ala Gly Ala Arg Gly Cys Arg Leu Arg Ser Gln  
35 40 45

Leu Val Pro Val Arg Ala Leu Gly Leu Gly His Arg Ser Asp Glu Leu  
50 55 60

Val Arg Phe Arg Phe Cys Ser Gly Ser Cys Arg Arg Ala Arg Ser Pro  
65 70 75 80

His Asp Leu Ser Leu Ala Ser Leu Leu Gly Ala Gly Ala Leu Arg Pro  
85 90 95

Pro Pro Gly Ser Arg Pro Val Ser Gln Pro Cys Cys Arg Pro Thr Arg  
100 105 110

Tyr Glu Ala Val Ser Phe Met Asp Val Asn Ser Thr Trp Arg Thr Val  
115 120 125

Asp Arg Leu Ser Ala Xaa Xaa Cys Gly Cys Leu Gly  
130 135 140

<210> 6

<211> 116

<212> PRT

<213> Homo sapiens

<220>

<223> Wherein Xaa at position 110 designates Asn or Thr,  
and Xaa at position 111 designates Ala or Pro

<400> 6

Ala Ala Arg Ala Gly Gly Pro Gly Asn Arg Ala Arg Ala Ala Gly Ala  
1 5 10 15

Arg Gly Cys Arg Leu Arg Ser Gln Leu Val Pro Val Arg Ala Leu Gly  
20 25 30

Leu Gly His Arg Ser Asp Glu Leu Val Arg Phe Arg Phe Cys Ser Gly  
35 40 45

Ser Cys Arg Arg Ala Arg Ser Pro His Asp Leu Ser Leu Ala Ser Leu  
 50 55 60

Leu Gly Ala Gly Ala Leu Arg Pro Pro Pro Gly Ser Arg Pro Val Ser  
 65 70 75 80

Gln Pro Cys Cys Arg Pro Thr Arg Tyr Glu Ala Val Ser Phe Met Asp  
 85 90 95

Val Asn Ser Thr Trp Arg Thr Val Asp Arg Leu Ser Ala Xaa Xaa Cys  
 100 105 110

Gly Cys Leu Gly  
 115

<210> 7

<211> 113

<212> PRT

<213> Homo sapiens

<210>

<213> Wherein Xaa at position 107 designates Asn or Thr,  
 and Xaa at position 108 designates Ala or Pro

<400> 7

Ala Gly Gly Pro Gly Asn Arg Ala Arg Ala Ala Gly Ala Arg Gly Cys  
 1 5 10 15

Arg Leu Arg Ser Gln Leu Val Pro Val Arg Ala Leu Gly Leu Gly His  
 20 25 30

Arg Ser Asp Glu Leu Val Arg Phe Arg Phe Cys Ser Gly Ser Cys Arg  
 35 40 45

Arg Ala Arg Ser Pro His Asp Leu Ser Leu Ala Ser Leu Leu Gly Ala  
 50 55 60

Gly Ala Leu Arg Pro Pro Pro Gly Ser Arg Pro Val Ser Gln Pro Cys  
 65 70 75 80

Cys Arg Pro Thr Arg Tyr Glu Ala Val Ser Phe Met Asp Val Asn Ser  
 85 90 95

Thr Trp Arg Thr Val Asp Arg Leu Ser Ala Xaa Xaa Cys Gly Cys Leu  
 100 105 110

Gly

<210> 8  
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<223> DISULFID: Gly43-Gly108 disulfide bridge

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<201> misc\_structure  
 <202> (595)..(705)  
 <203> DISULFID: Gly70-Gly136 disulfide bridge

<200>  
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 <202> (517)..(711)  
 <203> DISULFID: Gly74-Gly138 disulfide bridge

<200>  
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 <202> (616)..(613)  
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 bridge

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 agggaggggtgg gggaacagct caacaatggc tgateggggc tctgtgtgtt gatagag 57

atg gaa ctt gga ctt gga ggc ctc tcc aag ctg tcc cac tgc ccc tgg 105  
 Met Glu Leu Gly Leu Gly Gly Leu Ser Thr Leu Ser His Cys Pro Trp  
 -30 -75 -70 -65

cct agg cgg cag cct gcc ctg tgg ccc acc ctg gcc gct ctg gct ctg 153  
 Pro Arg Arg Gln Pro Ala Leu Trp Pro Thr Leu Ala Ala Leu Ala Leu  
 -60 -55 -50

ctg agc agc gtc gca gag gcc tcc ctg ggc tcc gag ccc cgc agc cct 201  
 Leu Ser Ser Val Ala Glu Ala Ser Leu Gly Ser Ala Pro Arg Ser Pro  
 -45 -40 -35

gcc ccc cgc gaa ggc ccc ccg cct gtc ctg gag tcc ccc gcc ggc cac 249  
 Ala Pro Arg Glu Gly Pro Pro Pro Val Leu Ala Ser Pro Ala Gly His  
 -30 -25 -20

ctg ccg ggg gga cgc aag gcc cgc tgg tgc agt gga aga gcc cgg cgg 297  
 Leu Pro Gly Gly Arg Thr Ala Arg Trp Cys Ser Gly Arg Ala Arg Arg  
 -15 -10 -5 -1

ccg ccg ccg cag cct tct cgg ccc gag ccc ccg ccg cct gca ccc cca 345  
 Pro Pro Pro Gln Pro Ser Arg Pro Ala Pro Pro Pro Pro Ala Pro Pro  
 1 5 10 15

tct gct ctt ccc cgc ggg ggc cgc gag ggc cgg gct ggg ggc ccg ggc 393  
 Ser Ala Leu Pro Arg Gly Gly Arg Ala Ala Arg Ala Gly Gly Pro Gly  
 20 25 30

agc cgc gct cgg gca ggc ggg gag cgg ggc tgc cgc ctg cgc tgc cag 441  
 Ser Arg Ala Arg Ala Ala Gly Ala Arg Gly Cys Arg Leu Arg Ser Gln

35

40

45

ctg gtg cgg gtg cgc ggc ctc ggc ctg ggc cac cgc tcc gac gag ctg 489  
 Leu Val Pro Val Arg Ala Leu Gly Leu Gly His Arg Ser Asp Glu Leu  
 50 55 60

gtg cgt ttc cgc ttc tgc agc ggc tcc tgc cgc cgc ggc cgc tct cca 537  
 Val Arg Phe Arg Phe Cys Ser Gly Ser Cys Arg Arg Ala Arg Ser Pro  
 65 70 75 80

cac gac ctc agc ctg gcc agc cta ctg ggc gcc ggc gcc ctg cga cgg 585  
 His Asp Leu Ser Leu Ala Ser Leu Leu Gly Ala Gly Ala Leu Arg Pro  
 85 90 95

ccc cgg ggc tcc cgg ccc gtc agc cag ccc tgc tgc cga ccc acg cgc 633  
 Pro Pro Gly Ser Arg Pro Val Ser Gln Pro Cys Cys Arg Pro Thr Arg  
 100 105 110

tac gaa gag gtc tcc ttc atg gac gtc aac agc acc tgg aga acc gtg 681  
 Tyr Glu Ala Val Ser Phe Met Asp Val Asn Ser Thr Trp Arg Thr Val  
 115 120 125

gac cgc ctc tcc gcc acc gcc tgc ggc tgc ctg ggc tgagggctcg 727  
 Asp Arg Leu Ser Ala Thr Ala Cys Gly Cys Leu Gly  
 130 135 140

ctccagggct ttgcagactg gacccctacc ggtggctctt cctgcctggg accctccgc 787

agagtccac tagccagcgg cctcagccag ggacgaaggc ctcaaagctg agaggccct 847

acgggtgggt gatg 861

<210> 9

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<212> FRT

<213> Homo sapiens

<400> 9

Met Glu Leu Gly Leu Gly Gly Leu Ser Thr Leu Ser His Cys Pro Trp  
 -80 -75 -70 -65

Pro Arg Arg Gln Pro Ala Leu Trp Pro Thr Leu Ala Ala Leu Ala Leu  
 -60 -55 -50

Leu Ser Ser Val Ala Glu Ala Ser Leu Gly Ser Ala Pro Arg Ser Pro  
 -45 -40 -35

Ala Pro Arg Glu Gly Pro Pro Pro Val Leu Ala Ser Pro Ala Gly His  
 -30 -25 -20

Leu Pro Gly Gly Arg Thr Ala Arg Trp Cys Ser Gly Arg Ala Arg Arg  
 -15 -10 -5 -1

Pro Pro Pro Gln Pro Ser Arg Pro Ala Pro Pro Pro Pro Ala Pro Pro  
 1 5 10 15

Ser Ala Leu Pro Arg Gly Gly Arg Ala Ala Arg Ala Gly Gly Pro Gly  
 20 25 30

Ser Arg Ala Arg Ala Ala Gly Ala Arg Gly Cys Arg Leu Arg Ser Gln  
 35 40 45

Leu Val Pro Val Arg Ala Leu Gly Leu Gly His Arg Ser Asp Glu Leu  
 50 55 60

Val Arg Phe Arg Phe Cys Ser Gly Ser Cys Arg Arg Ala Arg Ser Pro  
 65 70 75 80

His Asp Leu Ser Leu Ala Ser Leu Leu Gly Ala Gly Ala Leu Arg Pro  
 85 90 95

Pro Pro Gly Ser Arg Pro Val Ser Gln Pro Cys Cys Arg Pro Thr Arg  
 100 105 110

Tyr Glu Ala Val Ser Phe Met Asp Val Asn Ser Thr Trp Arg Thr Val  
 115 120 125

Asp Arg Leu Ser Ala Thr Ala Cys Gly Cys Leu Gly  
 130 135 140

02100 10

02110 140

02120 PRT

02130 Homo sapiens

02200

02210 CARBOHYD

02220 (122)

02230 glycosylated asparagine

04000 10

Pro Pro Pro Gln Pro Ser Arg Pro Ala Pro Pro Pro Pro Ala Pro Pro  
 1 5 10 15

Ser Ala Leu Pro Arg Gly Gly Arg Ala Ala Arg Ala Gly Gly Pro Gly  
20 25 30

Ser Arg Ala Arg Ala Ala Gly Ala Arg Gly Cys Arg Leu Arg Ser Gln  
35 40 45

Leu Val Pro Val Arg Ala Leu Gly Leu Gly His Arg Ser Asp Glu Leu  
50 55 60

Val Arg Phe Arg Phe Cys Ser Gly Ser Cys Arg Arg Ala Arg Ser Pro  
65 70 75 80

His Asp Leu Ser Leu Ala Ser Leu Leu Gly Ala Gly Ala Leu Arg Pro  
85 90 95

Pro Pro Gly Ser Arg Pro Val Ser Gln Pro Cys Cys Arg Pro Thr Arg  
100 105 110

Tyr Glu Ala Val Ser Phe Met Asp Val Asn Ser Thr Trp Arg Thr Val  
115 120 125

Asp Arg Leu Ser Ala Thr Ala Cys Gly Cys Leu Gly  
130 135 140

<110> 11

<111> 116

<112> PRT

<113> Homo sapiens

<120>

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<122> (93)

<123> glycosylated asparagine

<400> 11

Ala Ala Arg Ala Gly Gly Pro Gly Ser Arg Ala Arg Ala Ala Gly Ala  
1 5 10 15

Arg Gly Cys Arg Leu Arg Ser Gln Leu Val Pro Val Arg Ala Leu Gly  
20 25 30

Leu Gly His Arg Ser Asp Glu Leu Val Arg Phe Arg Phe Cys Ser Gly  
35 40 45

Ser Cys Arg Arg Ala Arg Ser Pro His Asp Leu Ser Leu Ala Ser Leu  
50 55 60

Leu Gly Ala Gly Ala Leu Arg Pro Pro Pro Gly Ser Arg Pro Val Ser  
65 70 75 80

Gln Pro Cys Cys Arg Pro Thr Arg Tyr Glu Ala Val Ser Phe Met Asp  
85 90 95

Val Asn Ser Thr Trp Arg Thr Val Asp Arg Leu Ser Ala Thr Ala Cys  
100 105 110

Gly Cys Leu Gly  
115

<210> 12

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<212> PRT

<213> Homo sapiens

<220>

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<222> (95)

<223> glycosylated asparagine

<400> 12

Ala Gly Gly Pro Gly Ser Arg Ala Arg Ala Ala Gly Ala Arg Gly Cys  
1 5 10 15

Arg Leu Arg Ser Gln Leu Val Pro Val Arg Ala Leu Gly Leu Gly His  
20 25 30

Arg Ser Asp Glu Leu Val Arg Phe Arg Phe Cys Ser Gly Ser Cys Arg  
35 40 45

Arg Ala Arg Ser Pro His Asp Leu Ser Leu Ala Ser Leu Leu Gly Ala  
50 55 60

Gly Ala Leu Arg Pro Pro Pro Gly Ser Arg Pro Val Ser Gln Pro Cys  
65 70 75 80

Cys Arg Pro Thr Arg Tyr Glu Ala Val Ser Phe Met Asp Val Asn Ser  
85 90 95

Thr Trp Arg Thr Val Asp Arg Leu Ser Ala Thr Ala Cys Gly Cys Leu  
100 105 110

Gly



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 ccaggccagc ctactgggag ccggggccct ggcacggccc ccgggtccc ggcccgtcag 60  
 ccagccctgc tgcggaccca ccggtacga agcgggtccc tt 102

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 <212> DNA  
 <213> Murinae gen. sp.

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 ccctccagc agcatctcag tctggccagc ctactgggag ctggggccct acggtccct 120  
 ccgggtccc ggccgatcag ccagccctgc tgcgggcca ctgcctatga ggccgtccc 180  
 ttcctggag tgaacagcac ctggagaaac gtggacggc 220

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 cggatccga gggcggagc ggcaggtgag cctgaaagg tggggcggg cggggcgct 180  
 ctgggcccc cccgggata tggtagccc ggggtcggaa ttgacacc gacggcgcg 240  
 ggcaggagc tctgaggga tggattggg ctggccccc agatgggccc ccgggctct 300  
 ggcagcaaca agtccctgg gccccagccc cctgtggac tggggttgg agccctgac 360  
 ccaaggcac agacgggtg ccaaggccc acttttaact aaaagaggc ctggcaggtg 420

cacaactctg ggcattgatcc acttgagctt cgggggaaag ccagcactg gtcccaggag 480  
 agggccttag aaggatacgg accaggaccc ctttggtatg gaggtaacgc tgagcatgga 540  
 gtggaaggaa cccagttac taattttctcc aaccacctg gtaccttcag cctgaagta 600  
 cagagcagaa ggttcttaga agacaggacc acagctgtgt gaggctcccc cctgaggcct 660  
 tagacgatct ctgagctcag ctgagctttg ttgcccata tggagaagtg agccattgat 720  
 tgaccttggt gcatcgcaaa ggaacaggtc ctgccaagca cctaaccacg agagcaaggt 780  
 tctccatcgc agctacgct gctgagttga ctctagctac tccaacctcc tgggtcgttt 840  
 cgagagactg gaggggaagg aggaataccc caaaggataa ctaactcact ttccagtttg 900  
 caagctgccc caggaaaggg gtggggaaac ggggtccacg aggtctctga tgggagcttc 960

tggagccgaa agct atg gaa ctg gga ctt gca gag cct act gca ttg tcc 1010  
 Met Glu Leu Gly Leu Ala Glu Pro Thr Ala Leu Ser  
 1 5 10

cag tgc ctg cgg cct agg tgg cag tca gcc tgg tgg cca acc cta gct 1058  
 His Cys Leu Arg Pro Arg Trp Gln Ser Ala Trp Trp Pro Thr Leu Ala  
 15 20 25

gtt cta gcc ctg ctg agc tgc gtc aca gaa gct tcc ctg gac cca atg 1106  
 Val Leu Ala Leu Leu Ser Cys Val Thr Glu Ala Ser Leu Asp Pro Met  
 30 35 40

tcc cgc agc ccc gcc gct cgc gac ggt ccc tca ccg gtc ttg gcg ccc 1154  
 Ser Arg Ser Pro Ala Ala Arg Asp Gly Pro Ser Pro Val Leu Ala Pro  
 45 50 55 60

ccc acg gac cag ctg cct ggg gga cag act gcg cat ttg tgc agc gaa 1202  
 Pro Thr Asp His Leu Pro Gly Gly His Thr Ala His Leu Cys Ser Glu  
 65 70 75

aga acc ctg cga ccc ccg cct cag tct cct cag ccc gca ccc ccg ccg 1250  
 Arg Thr Leu Arg Pro Pro Pro Gln Ser Pro Gln Pro Ala Pro Pro Pro  
 80 85 90

cct ggt ccc gcg ctg cag tct cct ccc gct gcg ctg cgc ggg gca cgc 1298  
 Pro Gly Pro Ala Leu Gln Ser Pro Pro Ala Ala Leu Arg Gly Ala Arg  
 95 100 105

gcg gcg cgt gca gga acc ccg agc agc cgc gca ccg acc aca gat gcg 1346  
 Ala Ala Arg Ala Gly Thr Arg Ser Ser Arg Ala Arg Thr Thr Asp Ala

110

115

120

ogc ggc tgc cgc ctg cgc tog cag ctg gtg ccg gtg agc ggc ctc ggc 1394  
 Arg Gly Cys Arg Leu Arg Ser Gln Leu Val Pro Val Ser Ala Leu Gly  
 125 130 135 140

cta ggc cac agc tcc gac gag ctg ata cgt ttc cgc ttc tgc agc ggc 1442  
 Leu Gly His Ser Ser Asp Glu Leu Ile Arg Phe Arg Phe Cys Ser Gly  
 145 150 155

tog tgc cgc cga gca cgc tcc cag cac gat ctc agt ctg gcc agc cta 1490  
 Ser Cys Arg Arg Ala Arg Ser Gln His Asp Leu Ser Leu Ala Ser Leu  
 160 165 170

ctg ggc gct ggc gcc cta cgc tog cct ccc ggc tcc cgc ccg atc agc 1538  
 Leu Gly Ala Gly Ala Leu Arg Ser Pro Pro Gly Ser Arg Pro Ile Ser  
 175 180 185

cag ccc tgc tgc cgc ccc act cgc tat gag gcc gtc tcc ttc atg gac 1586  
 Gln Pro Cys Cys Arg Pro Thr Arg Tyr Glu Ala Val Ser Phe Met Asp  
 190 195 200

gtg aac agc acc tgg agg acc gtg gac cac ctc tcc gcc act gcc tgc 1634  
 Val Asn Ser Thr Trp Arg Thr Val Asp His Leu Ser Ala Thr Ala Cys  
 205 210 215 220

ggc tgt ctg ggc tgaggatgat ctatctccaa gcttttgcac actagaccaa 1686  
 Gly Cys Leu Gly

tctgttgccc taactgggaa agctccaccc ggcctcacta accaggagcc tcaactcagc 1746

aggatatgga ggcctgcagag ctcaggccccc aggcgggtga gtgacagacg togtoggcat 1806

gacagacaga gtgaaagatg toggaaacac tgaccaacag tcccaagttg ttcattggatc 1866

ccagctctac agacaggaga aacctcagct aaagagaact cctctgggag aatccagaaa 1926

tggccctctg tccctggggaa tgaattttga agagatatat atacatatat acattgtagt 1986

ccggttctg gaccagcctg tgcagaaacc agtcgggtgt tcacttctgg aagccgaagc 2046

cctatttatt atttctaaat tatttattta ctttgaaaaa aaacggccaa gtgggcctcc 2106

ctttagtgag ggttaatttg tgatccggg 2136

210> 16

211> 224

<212> PRT

<213> Murinae gen. sp.

<400> 16

Met Glu Leu Gly Leu Ala Glu Pro Thr Ala Leu Ser His Cys Leu Arg  
1 5 10 15

Pro Arg Trp Gln Ser Ala Trp Trp Pro Thr Leu Ala Val Leu Ala Leu  
20 25 30

Leu Ser Cys Val Thr Glu Ala Ser Leu Asp Pro Met Ser Arg Ser Pro  
35 40 45

Ala Ala Arg Asp Gly Pro Ser Pro Val Leu Ala Pro Pro Thr Asp His  
50 55 60

Leu Pro Gly Gly His Thr Ala His Leu Cys Ser Glu Arg Thr Leu Arg  
65 70 75 80

Pro Pro Pro Gln Ser Pro Gln Pro Ala Pro Pro Pro Pro Gly Pro Ala  
85 90 95

Leu Gln Ser Pro Pro Ala Ala Leu Arg Gly Ala Arg Ala Ala Arg Ala  
100 105 110

Gly Thr Arg Ser Ser Arg Ala Arg Thr Thr Asp Ala Arg Gly Cys Arg  
115 120 125

Leu Arg Ser Gln Leu Val Pro Val Ser Ala Leu Gly Leu Gly His Ser  
130 135 140

Ser Asp Glu Leu Ile Arg Phe Arg Phe Cys Ser Gly Ser Cys Arg Arg  
145 150 155 160

Ala Arg Ser Gln His Asp Leu Ser Leu Ala Ser Leu Leu Gly Ala Gly  
165 170 175

Ala Leu Arg Ser Pro Pro Gly Ser Arg Pro Ile Ser Gln Pro Cys Cys  
180 185 190

Arg Pro Thr Arg Tyr Glu Ala Val Ser Phe Met Asp Val Asn Ser Thr  
195 200 205

Trp Arg Thr Val Asp His Leu Ser Ala Thr Ala Cys Gly Cys Leu Gly  
210 215 220

<210> 17  
<211> 13  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR Primer

<400> 17  
cctggccagc ctactggg 18

<210> 18  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR Primer

<400> 18  
aaggagacgg ctctgtatgg 20

<210> 19  
<211> 17  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR Primer

<400> 19  
atgggaacttg gacttgg 17

<210> 20  
<211> 16  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR Primer

<400> 20  
tccatcaccc accggc 16

<210> 21  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR Primer

<400> 21  
gggcacccgt cgcacgag 18

<210> 22  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR Primer

<400> 22  
ggcggtccac ggttctcag 20

<210> 23  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR Primer

<400> 23  
ccaagccac ctgggtgccc tctttctcc 29

<210> 24  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR Primer

<400> 24  
catcacccac cggcaggggc ctctcag 27

<210> 25  
 <211> 37  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: PCR Primer

<400> 35  
 gaggcacgc cggcctgat ctcagccga ggaca 35

<210> 26  
 <211> 34  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: PCR Primer

<400> 26  
 cctggctga ggccgtggc tagtgggact ctgc 34

<210> 27  
 <211> 31  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Hykridization  
 Probe

<400> 27  
 ncaggtgct cgtggggggc gccagaaccg g 31

<210> 18  
 <211> 16  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: PCR primer

<400> 28  
 ctaggagcc atgccc 16

<210> 29  
 <211> 351  
 <212> DNA  
 <213> Homo sapiens

<400> 29  
 atggttgtag gacggggatc tegtgttgtt gcagcaggag caggtgggtg tegtgttgtt 60  
 tctcaactag tggcgggtgg tgcactcgga ctgggacacc gtcccgacga actagtacgt 120  
 ttctgttttt gttcaggatc ttgttgttgt gcacgtttct cgcctgatct atctctagca 180  
 tctctactag gagcgggagc actaagaccc cggcggggat ctagacctgt atctcaacct 240  
 tgttgtagac ctactagata cgaagcagta tctttcatgg acgtaaaact tacatggaga 300  
 accgttagata gactatctgc aacgcgatgt ggtgtgtctg gatgataata g 351

<210> 30  
 <211> 414  
 <212> DNA  
 <213> Homo sapiens

<400> 30  
 atggggccatc atcctcatca tcatcctcat cctcactcga gggggccatc cgaacgacga 60  
 gacaagggtg gaggaacggg atcttgttgt cgtgcagcag gagcaagtggt ctgttgttgt 120  
 cgtttctaac tagtgcgggt ggttgcactc ggcctgggac accgttcoga cgaactagta 180  
 cgttttgttt ttgttccagg atcttgttgt cgtgcacgtt ctccgcctga tctatctcta 240  
 gcatctctac taggagccgg agcactaaga cggcggcggg gatctagacc tgtatctcaa 300  
 ccttgtttgt gacctactag atacgaagca gtatctttca tggacgtaaa ctctacatgg 360  
 agaaccgtag atagactatc tgcaacogca tgtggtgtgc taggatgata atag 414

<210> 31  
 <211> 39  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: PCR primer

<400> 31  
 aaggaaaaaa ggcgcgcgca tggaaattgg atttggagg 39

<210> 32  
 <211> 39  
 <212> DNA  
 <213> Artificial Sequence

<220>



<223> Description of Artificial Sequence: PCR primer

<400> 32

ttttttcttt ggaggcgcgt cagccagggc agccgcagg

39

<210> 33

<211> 16

<212> DNA

<213> Artificial Sequence

<210>

<213> Description of Artificial Sequence: primer

<400> 33

gagcagccc tcagcc

16

<210> 34

<211> 224

<212> PRT

<213> Rattus sp.

<400> 34

Met Glu Leu Gly Leu Gly Glu Pro Thr Ala Leu Ser His Cys Leu Arg

1

5

10

15

Pro Arg Trp Gln Pro Ala Leu Trp Pro Thr Leu Ala Ala Leu Ala Leu

20

25

30

Leu Ser Ser Val Thr Glu Ala Ser Leu Asp Pro Met Ser Arg Ser Pro

35

40

45

Ala Ser Arg Asp Val Pro Ser Pro Val Leu Ala Pro Pro Thr Asp Tyr

50

55

60

Leu Pro Gly Gly His Thr Ala His Leu Cys Ser Glu Arg Ala Leu Arg

65

70

75

80

Pro Pro Pro Gln Ser Pro Gln Pro Ala Pro Pro Pro Pro Gly Pro Ala

85

90

95

Leu Gln Ser Pro Pro Ala Ala Leu Arg Gly Ala Arg Ala Ala Arg Ala

100

105

110

Gly Thr Arg Ser Ser Arg Ala Arg Ala Thr Asp Ala Arg Gly Cys Arg

115

120

125

Leu Arg Ser Gln Leu Val Pro Val Ser Ala Leu Gly Leu Gly His Ser  
130 135 140

Ser Asp Glu Leu Ile Arg Phe Arg Phe Cys Ser Gly Ser Cys Arg Arg  
145 150 155 160

Ala Arg Ser Pro His Asp Leu Ser Leu Ala Ser Leu Leu Gly Ala Gly  
165 170 175

Ala Leu Arg Ser Pro Pro Gly Ser Arg Pro Ile Ser Gln Pro Cys Cys  
180 185 190

Arg Pro Thr Arg Tyr Glu Ala Val Ser Phe Met Asp Val Asn Ser Thr  
195 200 205

Trp Arg Thr Val Asp His Leu Ser Ala Thr Ala Cys Gly Cys Leu Gly  
210 215 220

<210> 35

<211> 365

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic gene  
for Neublabin

<400> 35

taccatggct ggaggacgg gatctcgtgc tcgtgcagca ggagcacgtg gctgtcgtct 60  
gggtctcaca ctagtgcggg tgcgtgcaat cggactggga cacggttcgg accgaactagt 120  
acgttttcgt ttttggtcag gatcttgctg tcgtgcacgt tctcggcatg atctatctct 180  
agpatctcta ctaggagcgg gagcaactaag accgcgcgcg ggatctagac ctgtatctca 240  
accttggtgt agactacta gatacgaagc agtatcttct atggacgtaa actctacatg 300  
gagaacgta gatagactat ctgcaacgc atgtggctgt ctaggatgat aatagggatc 360  
cgtct 365

<210> 36

<211> 365

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic gene

for Neublabin

<400> 36

```
atgggtacga cctcctggcc ctagagcaag agcaagtcgt cctcgtgcac cgacagcaga 60
cgcaagagtt gatcaaggcc acgcacgtga gctgaccct gtggcaagga tgcttgatca 120
tgcaaaaagca aaaacaagtc ctagaacaga agcaagtgca agaggcgtac tagatagaga 180
tcgtagagat gatcctgggc ctcgtgattc tggcgggggc cctagatctg gacatagagt 240
tggaacaaca totggatgat ctatgcttgg tcatagaaaag tacctgcatt tgagatgtac 300
ctcttggcat ctatctgata gacgttgggc tacacgcaga gatcctaata ttatcctag 360
gcaga
```

<410> 37

<411> 114

<412> PRT

<413> Artificial Sequence

<420>

<423> Description of Artificial Sequence:synthetic  
Neublabin

<400> 37

```
Met Ala Gly Gly Pro Gly Ser Arg Ala Arg Ala Ala Gly Ala Arg Gly
  1           5           10          15
```

```
Cys Arg Leu Arg Ser Gln Leu Val Pro Val Arg Ala Leu Gly Leu Gly
      20           25           30
```

```
His Arg Ser Asp Glu Leu Val Arg Phe Arg Phe Cys Ser Gly Ser Cys
      35           40           45
```

```
Arg Arg Ala Arg Ser Pro His Asp Leu Ser Leu Ala Ser Leu Leu Gly
      50           55           60
```

```
Ala Gly Ala Leu Arg Pro Pro Pro Gly Ser Arg Pro Val Ser Gln Pro
      65           70           75           80
```

```
Cys Cys Arg Pro Thr Arg Tyr Glu Ala Val Ser Phe Met Asp Val Asn
      85           90           95
```

```
Ser Thr Trp Arg Thr Val Asp Arg Leu Ser Ala Thr Ala Cys Gly Cys
     100          105          110
```

Leu Gly

<410> 38

4211 - 442  
4212 - DNA  
4213 - Artificial Sequence

4220 -  
4223 - Description of Artificial Sequence:synthetic gene  
gene for HisNeublastin

4400 - 38  
tactatgggc catcatcacc atcaccatca tcatcatcac tcgagcgggc atatcgacga 60  
cgagagacaag gatggaggac cgggatctcg tgcctgtgca gcaggagcac gtggctgtcg 120  
tcctcgttct caactagtgc cggtgogtgc actcggaact ggacacggtt ccgacgaact 180  
agtaagtttt cgtttttggt caggatcttg tgcctgtgca cgttctccgc atgatctatc 240  
tctatpatct ctactaggag ccggagcaact aagacgcgcg ccgggatcta gacctgtatc 300  
tcacaccttg tgtagaacta ctagatacga agcagtatct ttcattggac taaactctac 360  
atggagaacc gtagatagac tatctgcaac cgcattgtgc tgtctaggat gataataggg 420  
atccggctgc taacaaagcc cg 442

4210 - 39  
4211 - 442  
4212 - DNA  
4213 - Artificial Sequence

4220 -  
4223 - Description of Artificial Sequence:synthetic gene  
for HisNeublastin

4400 - 39  
atggtaccgc gtagtagtag tagtagtagt agtagtagtg agctcgccgg tatagctgct 60  
gctgctgttc cgaacctctg gccctagagc acgagcaagt cgtcctctgt caccgacagc 120  
agacgcaaga gttgateacg gccacgcaag tgagcctgac cctgtggcaa ggcctgttga 180  
tcattgcaaa gcaaaaacaa gtcttagaac agcagcaagt gcaagaggcg tactagatag 240  
agatcgtaga gatgatectc gccctcgtga ttctggcggc gccctagat ctggacatag 300  
agttggaaca acatctggat gatctatgct tgcctataga aagtacctgc atttgagatg 360  
tacctcttgg catctatctg atagaogttg gcgtaacacg acagatctca ctattatccc 420  
taggcggacg attgtttcgg gc 442

4210 - 40  
4211 - 135  
4212 - FRT  
4213 - Artificial Sequence

4220 -  
4223 - Description of Artificial Sequence:synthetic  
HisNeublastin

<400> 40

Met Gly His His His His His His His His His Ser Ser Gly His  
1 5 10 15

Ile Asp Asp Asp Asp Lys Ala Gly Gly Pro Gly Ser Arg Ala Arg Ala  
20 25 30

Ala Gly Ala Arg Gly Cys Arg Leu Arg Ser Gln Leu Val Pro Val Arg  
35 40 45

Ala Leu Gly Leu Gly His Arg Ser Asp Glu Leu Val Arg Phe Arg Phe  
50 55 60

Cys Ser Gly Ser Cys Arg Arg Ala Arg Ser Pro His Asp Leu Ser Leu  
65 70 75 80

Ala Ser Leu Leu Gly Ala Gly Ala Leu Arg Pro Pro Pro Gly Ser Arg  
85 90 95

Pro Val Ser Gln Pro Cys Cys Arg Pro Thr Arg Tyr Glu Ala Val Ser  
100 105 110

Phe Met Asp Val Asn Ser Thr Trp Arg Thr Val Asp Arg Leu Ser Ala  
115 120 125

Thr Ala Cys Gly Cys Leu Gly  
130 135